



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/511,910

Source: PJT/10

Date Processed by STIC: 10/29/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents; P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202



PCT

*Suggestion: consult
Sequence Rules
for VALID format*

RAW SEQUENCE LISTING

DATE: 10/29/2004

PATENT APPLICATION: US/10/511,910

TIME: 11:30:20

Input Set : N:\FANTU\10511910.txt

Output Set: N:\CRF4\10292004\J511910.raw

2 <110> APPLICANT: Japan Science and Technology Corporation

3 <120> TITLE OF INVENTION: A method for detection of rheumatoid arthritis by detecting

the

4 upregulation of expression of WNT

5 <130> FILE REFERENCE: TAN-345

C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/511,910

C--> 6 <141> CURRENT FILING DATE: 2004-10-20

6 <160> NUMBER OF SEQ ID NOS: 44

errors throughout

**Does Not Comply
Corrected Diskette Needed**

ERRORED SEQUENCES

global error

7 <210> SEQ ID NO: 1

8 <211> LENGTH: 20

9 <212> TYPE: DNA

10 <213> ORGANISM: Artificial

W--> 11 <220> FEATURE:

W--> 11 <223> OTHER INFORMATION:

W--> 11 <400>1

E--> 12 5'-tcctgctcag aaggttccat

13 <210> SEQ ID NO: 2

14 <211> LENGTH: 20

15 <212> TYPE: DNA

16 <213> ORGANISM: Artificial

W--> 17 <220> FEATURE:

W--> 17 <223> OTHER INFORMATION:

W--> 17 <400>2

E--> 18 5'-gctgtacgtg cagaagttgg

19 <210> SEQ ID NO: 3

20 <211> LENGTH: 20

21 <212> TYPE: DNA

22 <213> ORGANISM: Artificial

W--> 23 <220> FEATURE:

W--> 23 <223> OTHER INFORMATION:

W--> 23 <400>3

E--> 24 5'-ctgtatcagg gaccgagagg

25 <210> SEQ ID NO: 4

26 <211> LENGTH: 20

27 <212> TYPE: DNA

28 <213> ORGANISM: Artificial

W--> 29 <220> FEATURE:

W--> 29 <223> OTHER INFORMATION:

W--> 29 <400>4

E--> 30 5'-caaagagaac tcgccaggag

*(213) Artificial needs explanation
in <220>-<223> section
(see p.5
for error
explanation)*

*20 ← insert cumulative
nucleotide total.
at right margin
insert of each line*

*do NOT show
prime marks or
dashes in the
sequences*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,910

DATE: 10/29/2004
TIME: 11:30:20

Input Set : N:\FANTU\10511910.txt
Output Set : N:\CRF4\10292004\J511910.raw

```
31 <210> SEQ ID NO: 5
32 <211> LENGTH: 20
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial
W--> 35 <220> FEATURE:
W--> 35 <223> OTHER INFORMATION:
W--> 35 <400>5
E--> 36 5'-actgagtgtg tgcagctgtg 20<
37 <210> SEQ ID NO: 6
38 <211> LENGTH: 20
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial
W--> 41 <220> FEATURE:
W--> 41 <223> OTHER INFORMATION:
W--> 41 <400>6
E--> 42 5'-tgatgtcttg ctgcagacac 20<
43 <210> SEQ ID NO: 7
44 <211> LENGTH: 20
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial
W--> 47 <220> FEATURE:
W--> 47 <223> OTHER INFORMATION:
W--> 47 <400>7
E--> 48 5'-acttcggcgt gtagtctcc 20<
49 <210> SEQ ID NO: 8
50 <211> LENGTH: 20
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial
W--> 53 <220> FEATURE:
W--> 53 <223> OTHER INFORMATION:
W--> 53 <400>8
E--> 54 5'-atttttcctt ccgcttctcc 20<
55 <210> SEQ ID NO: 9
56 <211> LENGTH: 20
57 <212> TYPE: DNA
58 <213> ORGANISM: Artificial
W--> 59 <220> FEATURE:
W--> 59 <223> OTHER INFORMATION:
W--> 59 <400>9
E--> 60 5'-ttgaggagtg ccactaccag 20<
61 <210> SEQ ID NO: 10
62 <211> LENGTH: 20
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial
W--> 65 <220> FEATURE:
W--> 65 <223> OTHER INFORMATION:
W--> 65 <400>10
E--> 66 5'-ctgaactgtg cgttgcgtgg 20<
67 <210> SEQ ID NO: 11
```

RAW SEQUENCE LISTING

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Input Set : N:\FANTU\10511910.txt

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```

68 <211> LENGTH: 20
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial
W--> 71 <220> FEATURE:
W--> 71 <223> OTHER INFORMATION:
W--> 71 <400>11
E--> 72 5'-cagttcaaga ccgtgcagac 20<
73 <210> SEQ ID NO: 12
74 <211> LENGTH: 20
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial
W--> 77 <220> FEATURE:
W--> 77 <223> OTHER INFORMATION:
W--> 77 <400>12
E--> 78 5'-cggaacctac ccacccata 20<
79 <210> SEQ ID NO: 13
80 <211> LENGTH: 20
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial
W--> 83 <220> FEATURE:
W--> 83 <223> OTHER INFORMATION:
W--> 83 <400>13
E--> 84 5'-gtgctgcttc gtcagggtga 20<
85 <210> SEQ ID NO: 14
86 <211> LENGTH: 20
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial
W--> 89 <220> FEATURE:
W--> 89 <223> OTHER INFORMATION:
W--> 89 <400>14
E--> 90 5'-cgagggttgaa gctgagttcc 20<
91 <210> SEQ ID NO: 15
92 <211> LENGTH: 20
93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial
W--> 95 <220> FEATURE:
W--> 95 <223> OTHER INFORMATION:
W--> 95 <400>15
E--> 96 5'-caactgcaca acaacgaggc 20<
97 <210> SEQ ID NO: 16
98 <211> LENGTH: 20
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial
W--> 101 <220> FEATURE:
W--> 101 <223> OTHER INFORMATION:
W--> 101 <400>16
E--> 102 5'-gtactacgca gcaccagtgg 20<
103 <210> SEQ ID NO: 17
104 <211> LENGTH: 20

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/511,910

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Input Set : N:\FANTU\10511910.txt

Output Set: N:\CRF4\10292004\J511910.raw

105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial
W--> 107 <220> FEATURE:
W--> 107 <223> OTHER INFORMATION:
W--> 107 <400>17
E--> 108 5'-gagaagcaag gccagtacca 20←
109 <210> SEQ ID NO: 18
110 <211> LENGTH: 20
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial
W--> 113 <220> FEATURE:
W--> 113 <223> OTHER INFORMATION:
W--> 113 <400>18
E--> 114 5'-acagcacatg aggtcacagc 20←
115 <210> SEQ ID NO: 19
116 <211> LENGTH: 20
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial
W--> 119 <220> FEATURE:
W--> 119 <223> OTHER INFORMATION:
W--> 119 <400>19
E--> 120 5'-acatgctatc agctctgctg 20←
121 <210> SEQ ID NO: 20
122 <211> LENGTH: 20
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial
W--> 125 <220> FEATURE:
W--> 125 <223> OTHER INFORMATION:
W--> 125 <400>20
E--> 126 5'-aaagatcagt tccgcctctg 20←

IMPORTANT

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

see pp 6,7 for more errors

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\FANTU\10511910.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27
Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44

err explanation

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27
Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44

delete quotation marks

10/5/20

6

Sequence Listing

<110> Japan Science and Technology Corporation

<120> A method for detection of rheumatoid arthritis by detecting the upregulation of expression of *WNT*

do NOT use italics
(use a fixed-width font)

10/511,911

7

<210>18
<211> 20
<212> DNA
<213> Artificial
<400>18
5'-acagcacatg aggtcacagc

<210>19
<211> 20
<212> DNA
<213> Artificial
<400>19

5'-acatgctatc agctctgctg

<210>20
<211> 20
<212> DNA
<213> Artificial
<400>20

5'-aaagatcagt tccgcctctg

<210>21
<211> 20
<212> DNA
<213> Artificial
<400>21

5'-gaaagtggca agctttggag

<210>22
<211> 20
<212> DNA
<213> Artificial
<400>22

5'-gaaagtggca agctttggag

<210>23
<211> 20
<212> DNA
<213> Artificial

<400>23

5'-aatgaggcttcacaacaacc

delete

insert a space

after each group of 10 nucleotides

(the above is a sample of global errors)

the
errors for
these are described
in previous pages

same errors

same

<220> insert
<223>

no explanation on
line

20< insert

VERIFICATION SUMMARY

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Input Set : N:\FANTU\10511910.txt

Output Set: N:\CRF4\10292004\J511910.raw

L:6 M:270 C: Current Application Number differs, Replaced Current Application No
 L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:11 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
 ORGANISM:Artificial
 L:11 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
 ORGANISM:Artificial
 L:11 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:11
 L:12 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:12 M:301 E: (44) No Sequence Data was Shown, SEQ ID:1
 L:12 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:1
 L:17 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
 ORGANISM:Artificial
 L:17 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
 ORGANISM:Artificial
 L:17 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:17
 L:18 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:18 M:301 E: (44) No Sequence Data was Shown, SEQ ID:2
 L:18 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:2
 L:23 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>
 ORGANISM:Artificial
 L:23 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
 ORGANISM:Artificial
 L:23 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:23
 L:24 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:24 M:301 E: (44) No Sequence Data was Shown, SEQ ID:3
 L:24 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:3
 L:29 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
 ORGANISM:Artificial
 L:29 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
 ORGANISM:Artificial
 L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:29
 L:30 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:30 M:301 E: (44) No Sequence Data was Shown, SEQ ID:4
 L:30 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:4
 L:35 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
 ORGANISM:Artificial
 L:35 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
 ORGANISM:Artificial
 L:35 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:35
 L:36 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:36 M:301 E: (44) No Sequence Data was Shown, SEQ ID:5
 L:36 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:5
 L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
 ORGANISM:Artificial
 L:41 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
 ORGANISM:Artificial
 L:41 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:41
 L:42 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:42 M:301 E: (44) No Sequence Data was Shown, SEQ ID:6
 L:42 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:6
 L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
 ORGANISM:Artificial
 L:47 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>

ORGANISM:Artificial

L:47 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:47

L:48 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2

L:48 M:301 E: (44) No Sequence Data was Shown, SEQ ID:7

L:48 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:7

L:53 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>

ORGANISM:Artificial

L:53 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>

ORGANISM:Artificial

L:53 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:53

L:54 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/511,910

DATE: 10/29/2004

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Input Set : N:\FANTU\10511910.txt

Output Set: N:\CRF4\10292004\J511910.raw

L:54 M:301 E: (44) No Sequence Data was Shown, SEQ ID:8
L:54 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:8
L:59 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial
L:59 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial
L:59 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:59
L:60 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:60 M:301 E: (44) No Sequence Data was Shown, SEQ ID:9
L:60 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:9
L:65 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial
L:65 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial
L:65 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:65
L:66 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:66 M:301 E: (44) No Sequence Data was Shown, SEQ ID:10
L:66 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:10
L:71 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial
L:71 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial
L:71 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:71
L:72 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:72 M:301 E: (44) No Sequence Data was Shown, SEQ ID:11
L:72 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:11
L:77 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
ORGANISM:Artificial
L:77 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:Artificial
L:77 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:77
L:78 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:78 M:301 E: (44) No Sequence Data was Shown, SEQ ID:12
L:78 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:12
L:83 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial
L:83 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial
L:83 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:83
L:84 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:84 M:301 E: (44) No Sequence Data was Shown, SEQ ID:13
L:84 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:13
L:89 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial
L:89 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial
L:89 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:89
L:90 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:90 M:301 E: (44) No Sequence Data was Shown, SEQ ID:14
L:90 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:14
L:95 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial
L:95 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>

ORGANISM:Artificial

L:95 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:95

L:96 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2

L:96 M:301 E: (44) No Sequence Data was Shown, SEQ ID:15

L:96 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:15

L:101 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>

ORGANISM:Artificial

L:101 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>

ORGANISM:Artificial

L:101 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:101

L:102 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2

L:102 M:301 E: (44) No Sequence Data was Shown, SEQ ID:16

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L:102 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:16
 L:107 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>
 ORGANISM:Artificial
 L:107 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
 ORGANISM:Artificial
 L:108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:108 M:301 E: (44) No Sequence Data was Shown, SEQ ID:17
 L:108 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:17
 L:114 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:114 M:301 E: (44) No Sequence Data was Shown, SEQ ID:18
 L:114 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:18
 L:120 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:120 M:301 E: (44) No Sequence Data was Shown, SEQ ID:19
 L:120 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:19
 L:126 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:126 M:301 E: (44) No Sequence Data was Shown, SEQ ID:20
 L:126 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:20
 L:132 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:132 M:301 E: (44) No Sequence Data was Shown, SEQ ID:21
 L:132 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:21
 L:138 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:138 M:301 E: (44) No Sequence Data was Shown, SEQ ID:22
 L:138 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:22
 L:144 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:144 M:301 E: (44) No Sequence Data was Shown, SEQ ID:23
 L:144 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:23
 L:150 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:150 M:301 E: (44) No Sequence Data was Shown, SEQ ID:24
 L:150 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:24
 L:156 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:156 M:301 E: (44) No Sequence Data was Shown, SEQ ID:25
 L:156 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:25
 L:162 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:162 M:301 E: (44) No Sequence Data was Shown, SEQ ID:26
 L:162 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:26
 L:168 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:168 M:301 E: (44) No Sequence Data was Shown, SEQ ID:27
 L:168 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:27
 L:174 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:174 M:301 E: (44) No Sequence Data was Shown, SEQ ID:28
 L:174 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:28
 L:180 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:180 M:301 E: (44) No Sequence Data was Shown, SEQ ID:29
 L:180 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:29
 L:186 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:186 M:301 E: (44) No Sequence Data was Shown, SEQ ID:30
 L:186 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:30
 L:192 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:192 M:301 E: (44) No Sequence Data was Shown, SEQ ID:31
 L:192 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:31
 L:198 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/511,910

DATE: 10/29/2004

TIME: 11:30:22

Input Set : N:\FANTU\10511910.txt

Output Set: N:\CRF4\10292004\J511910.raw

L:198 M:301 E: (44) No Sequence Data was Shown, SEQ ID:32
L:198 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:32
L:204 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:204 M:301 E: (44) No Sequence Data was Shown, SEQ ID:33
L:204 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:33
L:210 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:210 M:301 E: (44) No Sequence Data was Shown, SEQ ID:34
L:210 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:34
L:216 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:216 M:301 E: (44) No Sequence Data was Shown, SEQ ID:35
L:216 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:35
L:222 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:222 M:301 E: (44) No Sequence Data was Shown, SEQ ID:36
L:222 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:36
L:228 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:228 M:301 E: (44) No Sequence Data was Shown, SEQ ID:37
L:228 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:37
L:234 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:234 M:301 E: (44) No Sequence Data was Shown, SEQ ID:38
L:234 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:38
L:240 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:240 M:301 E: (44) No Sequence Data was Shown, SEQ ID:39
L:240 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:39
L:246 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:246 M:301 E: (44) No Sequence Data was Shown, SEQ ID:40
L:246 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:40
L:252 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:252 M:301 E: (44) No Sequence Data was Shown, SEQ ID:41
L:252 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:41
L:258 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:258 M:301 E: (44) No Sequence Data was Shown, SEQ ID:42
L:258 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:42
L:264 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:264 M:301 E: (44) No Sequence Data was Shown, SEQ ID:43
L:264 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:43
L:270 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44
L:278 M:301 E: (44) No Sequence Data was Shown, SEQ ID:44
L:278 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:0 SEQ:44